SEQUENCE LISTING

<110> Vadim R. Viviani
Yoshihiro Ohmiya

<120> Nucleic Acid Molecules Encoding Red and
Green Emitting Luciferases

<130> 2799.1001-001

<140> 09/516,958
<141> 2000-03-01

<150> 09/388,290
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gag cgt cct cgt gat ata gtc cat cct ggc tcg gca gga caa caa tta 100
Glu Arg Pro Arg Asp Ile Val His Pro Gly Ser Ala Gly Gln Gln Leu
10 15 20 25

tac caa tca ttg tat aaa ttt gca tct ttt cct gaa gca ata atc gat 148
Tyr Gln Ser Leu Tyr Lys Phe Ala Ser Phe Pro Glu Ala Ile Ile Asp
30 35 40

gct cat aca aat gaa gta ata tca tat gct caa ata ttt gaa acc agc 196
Ala His Thr Asn Glu Val Ile Ser Tyr Ala Gln Ile Phe Glu Thr Ser
45 50 55

tgc cgc tta gct gtt agt ata gaa caa tat ggc ttg aat gaa aac aat 244
Cys Arg Leu Ala Val Ser Ile Glu Gln Tyr Gly Leu Asn Glu Asn Asn
60 65 70

gtt gtg ggt gta tgc agt gaa aac aat ata aac ttt ttt aat cct gtc 292
Val Val Gly Val Cys Ser Glu Asn Asn Ile Asn Phe Phe Asn Pro Val
75 80 85

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ctt gct gct tta tac tta gga ata cca gta gca aca tca aat gat atg    340
Leu Ala Ala Leu Tyr Leu Gly Ile Pro Val Ala Thr Ser Asn Asp Met
 90                 95                 100                 105

tac aca gat gga gag tta act ggt cat ttg aat ata tca aaa cca act    388
Tyr Thr Asp Gly Glu Leu Thr Gly His Leu Asn Ile Ser Lys Pro Thr
                110                 115                 120

atc atg ttt agt tca aag aaa gca ctc ccg ctt att ctg aga gta cag    436
Ile Met Phe Ser Ser Lys Lys Ala Leu Pro Leu Ile Leu Arg Val Gln
            125                 130                 135

caa aat cta agt ttc att aaa aaa gtc gta gtt atc gat agc atg tac    484
Gln Asn Leu Ser Phe Ile Lys Lys Val Val Val Ile Asp Ser Met Tyr
        140                 145                 150

gac att aat ggc gtt gaa tgc gta tct acc ttt gtt gca cgt tat act    532
Asp Ile Asn Gly Val Glu Cys Val Ser Thr Phe Val Ala Arg Tyr Thr
    155                 160                 165

gac cac acc ttt gat cca ttg tca ttt aca cca aaa gat ttt gat ccc    580
Asp His Thr Phe Asp Pro Leu Ser Phe Thr Pro Lys Asp Phe Asp Pro
170                 175                 180                 185

ctt gaa aaa atc gca tta att atg tca tca tct gga aca act gga ttg    628
Leu Glu Lys Ile Ala Leu Ile Met Ser Ser Ser Gly Thr Thr Gly Leu
                190                 195                 200

cct aag ggt gta gta ctg agc cat aga agt cta act ata aga ttc gtt    676
Pro Lys Gly Val Val Leu Ser His Arg Ser Leu Thr Ile Arg Phe Val
            205                 210                 215

cat agc agg gat ccc att tat ggc act cgt acg gtt cca caa aca tca    724
His Ser Arg Asp Pro Ile Tyr Gly Thr Arg Thr Val Pro Gln Thr Ser
        220                 225                 230

att ctt tcc tta gta ccg ttc cat cat gcc ttt gga atg ttt act aca    772
Ile Leu Ser Leu Val Pro Phe His His Ala Phe Gly Met Phe Thr Thr
    235                 240                 245

tta tct tac ttt gta gta gga ctt aag gtt gta atg ttg aag aaa ttt    820
Leu Ser Tyr Phe Val Val Gly Leu Lys Val Val Met Leu Lys Lys Phe
250                 255                 260                 265

gag ggc gca ctt ttc tta aaa acc ata cag aat tac aaa atc ccc act    868
Glu Gly Ala Leu Phe Leu Lys Thr Ile Gln Asn Tyr Lys Ile Pro Thr
                270                 275                 280

att gta gtg gcc cct cca gtt atg gtg ttt ttg gct aaa agc cca tta    916
Ile Val Val Ala Pro Pro Val Met Val Phe Leu Ala Lys Ser Pro Leu
            285                 290                 295

gtc gat caa tac gat tta tcg agc tta acg gaa gtt gct act gga gga    964
Val Asp Gln Tyr Asp Leu Ser Ser Leu Thr Glu Val Ala Thr Gly Gly
        300                 305                 310

gct cct tta gga aaa gat gtc gca gaa gca gta gca aag agg ttg aaa   1012
Ala Pro Leu Gly Lys Asp Val Ala Glu Ala Val Ala Lys Arg Leu Lys
    315                 320                 325
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tta cct gga atc ata caa gga tat gga tta act gaa act tgc tgc gct    1060
Leu Pro Gly Ile Ile Gln Gly Tyr Gly Leu Thr Glu Thr Cys Cys Ala
330                 335                 340                 345

gta atg att acc cct cat aat gct gtg aaa aca ggt tca act gga aga    1108
Val Met Ile Thr Pro His Asn Ala Val Lys Thr Gly Ser Thr Gly Arg
                350                 355                 360

ccc ttg cca tac att aaa gct aaa gtt tta gat aac gct act ggg aag    1156
Pro Leu Pro Tyr Ile Lys Ala Lys Val Leu Asp Asn Ala Thr Gly Lys
            365                 370                 375

gcg cta gga cca gga gaa aga ggc gaa ata tgc ttt caa agt gaa atg    1204
Ala Leu Gly Pro Gly Glu Arg Gly Glu Ile Cys Phe Gln Ser Glu Met
        380                 385                 390

att atg aaa gga tat tac aac aat ccg gaa gca act att gat act att    1252
Ile Met Lys Gly Tyr Tyr Asn Asn Pro Glu Ala Thr Ile Asp Thr Ile
    395                 400                 405

gac aaa gat ggt tgg ctt cat tct gga gat att gga tat tac gac gaa    1300
Asp Lys Asp Gly Trp Leu His Ser Gly Asp Ile Gly Tyr Tyr Asp Glu
410                 415                 420                 425

gat gga aat ttc ttt ata gtt gat cga ttg aaa gaa ctt att aaa tac    1348
Asp Gly Asn Phe Phe Ile Val Asp Arg Leu Lys Glu Leu Ile Lys Tyr
                430                 435                 440

aag gga tat cag gtt gcg cct gct gaa ctg gaa aat ctg ctt tta caa    1396
Lys Gly Tyr Gln Val Ala Pro Ala Glu Leu Glu Asn Leu Leu Leu Gln
            445                 450                 455

cat cca agt att gct gat gcg ggt gtt act gga gtt ccg gac gaa ttt    1444
His Pro Ser Ile Ala Asp Ala Gly Val Thr Gly Val Pro Asp Glu Phe
        460                 465                 470

ggt gga caa tta cct gct gct tgt gtt gtg tta gaa tct ggc aag acg    1492
Gly Gly Gln Leu Pro Ala Ala Cys Val Val Leu Glu Ser Gly Lys Thr
    475                 480                 485

ctg act gaa aag gaa gtt caa gat ttt att gca gca caa gtc act cca    1540
Leu Thr Glu Lys Glu Val Gln Asp Phe Ile Ala Ala Gln Val Thr Pro
490                 495                 500                 505

aca aag cat ctt cga ggc ggt gtc gta ttt gta gac agt att ccg aaa    1588
Thr Lys His Leu Arg Gly Gly Val Val Phe Val Asp Ser Ile Pro Lys
                510                 515                 520

ggc cct act gga aaa ctc atc aga aag gag ctc cga gaa ata ttt gcc    1636
Gly Pro Thr Gly Lys Leu Ile Arg Lys Glu Leu Arg Glu Ile Phe Ala
            525                 530                 535

cag cga gca cca aaa tca aaa tta taagttcaat gtattgcttt agttctaaaa  1690
Gln Arg Ala Pro Lys Ser Lys Leu
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<213> Phrixothrix vivianii

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20 25 30
Ala Ser Phe Pro Glu Ala Ile Ile Asp Ala His Thr Asn Glu Val Ile
35 40 45
Ser Tyr Ala Gln Ile Phe Glu Thr Ser Cys Arg Leu Ala Val Ser Ile
50 55 60
Glu Gln Tyr Gly Leu Asn Glu Asn Asn Val Val Gly Val Cys Ser Glu
65 70 75 80
Asn Asn Ile Asn Phe Phe Asn Pro Val Leu Ala Ala Leu Tyr Leu Gly
85 90 95
Ile Pro Val Ala Thr Ser Asn Asp Met Tyr Thr Asp Gly Glu Leu Thr
100 105 110
Gly His Leu Asn Ile Ser Lys Pro Thr Ile Met Phe Ser Ser Lys Lys
115 120 125
Ala Leu Pro Leu Ile Leu Arg Val Gln Gln Asn Leu Ser Phe Ile Lys
130 135 140
Lys Val Val Val Ile Asp Ser Met Tyr Asp Ile Asn Gly Val Glu Cys
145 150 155 160
Val Ser Thr Phe Val Ala Arg Tyr Thr Asp His Thr Phe Asp Pro Leu
165 170 175
Ser Phe Thr Pro Lys Asp Phe Asp Pro Leu Glu Lys Ile Ala Leu Ile
180 185 190
Met Ser Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Val Leu Ser
195 200 205
His Arg Ser Leu Thr Ile Arg Phe Val His Ser Arg Asp Pro Ile Tyr
210 215 220
Gly Thr Arg Thr Val Pro Gln Thr Ser Ile Leu Ser Leu Val Pro Phe
225 230 235 240
His His Ala Phe Gly Met Phe Thr Thr Leu Ser Tyr Phe Val Val Gly
245 250 255
Leu Lys Val Val Met Leu Lys Lys Phe Glu Gly Ala Leu Phe Leu Lys
260 265 270
Thr Ile Gln Asn Tyr Lys Ile Pro Thr Ile Val Val Ala Pro Pro Val
275 280 285
Met Val Phe Leu Ala Lys Ser Pro Leu Val Asp Gln Tyr Asp Leu Ser
290 295 300
Ser Leu Thr Glu Val Ala Thr Gly Gly Ala Pro Leu Gly Lys Asp Val
305 310 315 320
Ala Glu Ala Val Ala Lys Arg Leu Lys Leu Pro Gly Ile Ile Gln Gly
325 330 335
Tyr Gly Leu Thr Glu Thr Cys Cys Ala Val Met Ile Thr Pro His Asn
340 345 350
Ala Val Lys Thr Gly Ser Thr Gly Arg Pro Leu Pro Tyr Ile Lys Ala
355 360 365
Lys Val Leu Asp Asn Ala Thr Gly Lys Ala Leu Gly Pro Gly Glu Arg
370 375 380
Gly Glu Ile Cys Phe Gln Ser Glu Met Ile Met Lys Gly Tyr Tyr Asn
385 390 395 400
Asn Pro Glu Ala Thr Ile Asp Thr Ile Asp Lys Asp Gly Trp Leu His
405 410 415

Ser Gly Asp Ile Gly Tyr Tyr Asp Glu Asp Gly Asn Phe Phe Ile Val
420 425 430
Asp Arg Leu Lys Glu Leu Ile Lys Tyr Lys Gly Tyr Gln Val Ala Pro
435 440 445
Ala Glu Leu Glu Asn Leu Leu Leu Gln His Pro Ser Ile Ala Asp Ala
450 455 460
Gly Val Thr Gly Val Pro Asp Glu Phe Gly Gly Gln Leu Pro Ala Ala
465 470 475 480
Cys Val Val Leu Glu Ser Gly Lys Thr Leu Thr Glu Lys Glu Val Gln
485 490 495
Asp Phe Ile Ala Ala Gln Val Thr Pro Thr Lys His Leu Arg Gly Gly
500 505 510
Val Val Phe Val Asp Ser Ile Pro Lys Gly Pro Thr Gly Lys Leu Ile
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530 535 540
Leu
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Val Val Asn Gly Asp Arg Pro Arg Asp Leu Val Phe Pro Gly Thr Ala
10 15 20

gga cta caa tta tat caa tca tta tat aaa tat tca tat att act gac 151
Gly Leu Gln Leu Tyr Gln Ser Leu Tyr Lys Tyr Ser Tyr Ile Thr Asp
25 30 35

gga ata atc gat gcc cat acc aat gaa gta ata tca tat gct caa ata 199
Gly Ile Ile Asp Ala His Thr Asn Glu Val Ile Ser Tyr Ala Gln Ile
40 45 50

ttt gaa acc agc tgc cgc ttg gca gtt agt cta gaa aaa tat ggc ttg 247
Phe Glu Thr Ser Cys Arg Leu Ala Val Ser Leu Glu Lys Tyr Gly Leu
55 60 65

gat cat aac aat gtt gtg gca ata tgc agt gaa aac aac ata cac ttt 295
Asp His Asn Asn Val Val Ala Ile Cys Ser Glu Asn Asn Ile His Phe
70 75 80 85

ttt ggc cct tta att gct gct tta tac caa gga ata cca atg gca aca 343
Phe Gly Pro Leu Ile Ala Ala Leu Tyr Gln Gly Ile Pro Met Ala Thr
90 95 100

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tca aat gat atg tac aca gaa agg gag atg att ggc cat ttg aat ata    391
Ser Asn Asp Met Tyr Thr Glu Arg Glu Met Ile Gly His Leu Asn Ile
            105                 110                 115

tcg aaa cca tgc ctt atg ttt tgt tca aag aaa tca ctc cca ttt att    439
Ser Lys Pro Cys Leu Met Phe Cys Ser Lys Lys Ser Leu Pro Phe Ile
        120                 125                 130

ctg aaa gta caa aaa cat cta gat ttc ctt aaa aga gtc ata gtc att    487
Leu Lys Val Gln Lys His Leu Asp Phe Leu Lys Arg Val Ile Val Ile
    135                 140                 145

gat agt atg tac gat atc aat ggc gtt gaa tgc gta ttt agc ttt gat    535
Asp Ser Met Tyr Asp Ile Asn Gly Val Glu Cys Val Phe Ser Phe Asp
150                 155                 160                 165

tca cgt aat act gat cac gcc ttt gat cca gtg aaa ttt aac cca aaa    583
Ser Arg Asn Thr Asp His Ala Phe Asp Pro Val Lys Phe Asn Pro Lys
                170                 175                 180

gag ttt gat ccc ttg gaa aga acc gca tta att atg aca tca tct gga    631
Glu Phe Asp Pro Leu Glu Arg Thr Ala Leu Ile Met Thr Ser Ser Gly
            185                 190                 195

aca act gga ttg cct aaa ggg gta gta ata agc cat aga agt ata act    679
Thr Thr Gly Leu Pro Lys Gly Val Val Ile Ser His Arg Ser Ile Thr
        200                 205                 210

ata aga ttc gtc cat agc agt gat ccc atc tat ggt act cgt att gct    727
Ile Arg Phe Val His Ser Ser Asp Pro Ile Tyr Gly Thr Arg Ile Ala
    215                 220                 225

cca gat aca tca att ctt gct ata gca ccg ttc cat cat gcc ttt gga    775
Pro Asp Thr Ser Ile Leu Ala Ile Ala Pro Phe His His Ala Phe Gly
230                 235                 240                 245

ctg ttt act gca cta gct tac ttt cca gta gga ctt aag att gta atg    823
Leu Phe Thr Ala Leu Ala Tyr Phe Pro Val Gly Leu Lys Ile Val Met
                250                 255                 260

gtg aag aaa ttt gag ggc gaa ttc ttc tta aaa acc ata caa aat tac    871
Val Lys Lys Phe Glu Gly Glu Phe Phe Leu Lys Thr Ile Gln Asn Tyr
            265                 270                 275

aaa atc gct tct att gta gtt cct cct cca att atg gta tat ttg gct    919
Lys Ile Ala Ser Ile Val Val Pro Pro Pro Ile Met Val Tyr Leu Ala
        280                 285                 290

aaa agt cca tta gtc gat gaa tac aat tgc tcg agc tta acg gaa att    967
Lys Ser Pro Leu Val Asp Glu Tyr Asn Cys Ser Ser Leu Thr Glu Ile
    295                 300                 305

gct agt gga ggc tct cct tta gga aga gat atc gca gat aaa gta gca   1015
Ala Ser Gly Gly Ser Pro Leu Gly Arg Asp Ile Ala Asp Lys Val Ala
310                 315                 320                 325

aag aga ttg aaa gta cat gga atc cta caa gga tat gga tta acc gaa   1063
Lys Arg Leu Lys Val His Gly Ile Leu Gln Gly Tyr Gly Leu Thr Glu
                330                 335                 340
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acc tgc agc gct cta ata ctt agc ccc aat gat cga gaa ctt aaa aaa    1111
Thr Cys Ser Ala Leu Ile Leu Ser Pro Asn Asp Arg Glu Leu Lys Lys
            345                 350                 355

ggt gca att gga acg cct atg cca tat gtt caa gtt aaa gtt ata gat    1159
Gly Ala Ile Gly Thr Pro Met Pro Tyr Val Gln Val Lys Val Ile Asp
        360                 365                 370

atc aat act ggg aag gcg cta gga cca aga gaa aaa ggc gaa ata tgc    1207
Ile Asn Thr Gly Lys Ala Leu Gly Pro Arg Glu Lys Gly Glu Ile Cys
    375                 380                 385

ttc aaa agt caa atg ctt atg aaa gga tat cac aac aat ccg caa gca    1255
Phe Lys Ser Gln Met Leu Met Lys Gly Tyr His Asn Asn Pro Gln Ala
390                 395                 400                 405

act cgt gat gct ctt gac aaa gat ggt tgg ctt cat act ggg gat ctt    1303
Thr Arg Asp Ala Leu Asp Lys Asp Gly Trp Leu His Thr Gly Asp Leu
                410                 415                 420

gga tat tac gac gaa gac aga ttt atc tat gta gtt gat cga ttg aaa    1351
Gly Tyr Tyr Asp Glu Asp Arg Phe Ile Tyr Val Val Asp Arg Leu Lys
            425                 430                 435

gaa ctt att aaa tat aaa gga tat cag gtt gcg cct gct gaa ctg gaa    1399
Glu Leu Ile Lys Tyr Lys Gly Tyr Gln Val Ala Pro Ala Glu Leu Glu
        440                 445                 450

aat ctg ctt tta caa cat cca aat att tct gat gcg ggt gtt att gaa    1447
Asn Leu Leu Leu Gln His Pro Asn Ile Ser Asp Ala Gly Val Ile Glu
    455                 460                 465

ttc cgg acg aat ttg ctg gtc aat tac ctt tcc gcg tgt gtt gtg tta    1495
Phe Arg Thr Asn Leu Leu Val Asn Tyr Leu Ser Ala Cys Val Val Leu
470                 475                 480                 485

gag cct ggt aag aca atg acc gaa aag gaa gtt cag gat tat att gca    1543
Glu Pro Gly Lys Thr Met Thr Glu Lys Glu Val Gln Asp Tyr Ile Ala
                490                 495                 500

gag cta gtc act aca act aaa cat ctt cga ggc ggt gtc gta ttt ata    1591
Glu Leu Val Thr Thr Thr Lys His Leu Arg Gly Gly Val Val Phe Ile
            505                 510                 515

gat agt att cca aaa ggc cca aca gga aaa ctc atg aga aac gaa ctc    1639
Asp Ser Ile Pro Lys Gly Pro Thr Gly Lys Leu Met Arg Asn Glu Leu
        520                 525                 530

cga gca ata ttt gcc cgg gaa cag gca aaa tca aaa tta taagctcaat     1688
Arg Ala Ile Phe Ala Arg Glu Gln Ala Lys Ser Lys Leu
    535                 540                 545

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agcctaaaaa aa                                                     1760
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20 25 30
Ser Tyr Ile Thr Asp Gly Ile Ile Asp Ala His Thr Asn Glu Val Ile
35 40 45
Ser Tyr Ala Gln Ile Phe Glu Thr Ser Cys Arg Leu Ala Val Ser Leu
50 55 60
Glu Lys Tyr Gly Leu Asp His Asn Asn Val Val Ala Ile Cys Ser Glu
65 70 75 80
Asn Asn Ile His Phe Phe Gly Pro Leu Ile Ala Ala Leu Tyr Gln Gly
85 90 95
Ile Pro Met Ala Thr Ser Asn Asp Met Tyr Thr Glu Arg Glu Met Ile
100 105 110
Gly His Leu Asn Ile Ser Lys Pro Cys Leu Met Phe Cys Ser Lys Lys
115 120 125
Ser Leu Pro Phe Ile Leu Lys Val Gln Lys His Leu Asp Phe Leu Lys
130 135 140
Arg Val Ile Val Ile Asp Ser Met Tyr Asp Ile Asn Gly Val Glu Cys
145 150 155 160
Val Phe Ser Phe Asp Ser Arg Asn Thr Asp His Ala Phe Asp Pro Val
165 170 175
Lys Phe Asn Pro Lys Glu Phe Asp Pro Leu Glu Arg Thr Ala Leu Ile
180 185 190
Met Thr Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Val Ile Ser
195 200 205
His Arg Ser Ile Thr Ile Arg Phe Val His Ser Ser Asp Pro Ile Tyr
210 215 220
Gly Thr Arg Ile Ala Pro Asp Thr Ser Ile Leu Ala Ile Ala Pro Phe
225 230 235 240
His His Ala Phe Gly Leu Phe Thr Ala Leu Ala Tyr Phe Pro Val Gly
245 250 255
Leu Lys Ile Val Met Val Lys Lys Phe Glu Gly Glu Phe Phe Leu Lys
260 265 270
Thr Ile Gln Asn Tyr Lys Ile Ala Ser Ile Val Val Pro Pro Pro Ile
275 280 285
Met Val Tyr Leu Ala Lys Ser Pro Leu Val Asp Glu Tyr Asn Cys Ser
290 295 300
Ser Leu Thr Glu Ile Ala Ser Gly Gly Ser Pro Leu Gly Arg Asp Ile
305 310 315 320
Ala Asp Lys Val Ala Lys Arg Leu Lys Val His Gly Ile Leu Gln Gly
325 330 335
Tyr Gly Leu Thr Glu Thr Cys Ser Ala Leu Ile Leu Ser Pro Asn Asp
340 345 350
Arg Glu Leu Lys Lys Gly Ala Ile Gly Thr Pro Met Pro Tyr Val Gln
355 360 365
Val Lys Val Ile Asp Ile Asn Thr Gly Lys Ala Leu Gly Pro Arg Glu
370 375 380
Lys Gly Glu Ile Cys Phe Lys Ser Gln Met Leu Met Lys Gly Tyr His
385 390 395 400
Asn Asn Pro Gln Ala Thr Arg Asp Ala Leu Asp Lys Asp Gly Trp Leu
405 410 415

His	Thr	Gly	Asp	Leu	Gly	Tyr	Tyr	Asp	Glu	Asp	Arg	Phe	Ile	Tyr	Val
			420					425					430		
Val	Asp	Arg	Leu	Lys	Glu	Leu	Ile	Lys	Tyr	Lys	Gly	Tyr	Gln	Val	Ala
		435					440					445			
Pro	Ala	Glu	Leu	Glu	Asn	Leu	Leu	Leu	Gln	His	Pro	Asn	Ile	Ser	Asp
	450					455					460				
Ala	Gly	Val	Ile	Glu	Phe	Arg	Thr	Asn	Leu	Leu	Val	Asn	Tyr	Leu	Ser
465					470					475					480
Ala	Cys	Val	Val	Leu	Glu	Pro	Gly	Lys	Thr	Met	Thr	Glu	Lys	Glu	Val
				485					490					495	
Gln	Asp	Tyr	Ile	Ala	Glu	Leu	Val	Thr	Thr	Thr	Lys	His	Leu	Arg	Gly
			500					505					510		
Gly	Val	Val	Phe	Ile	Asp	Ser	Ile	Pro	Lys	Gly	Pro	Thr	Gly	Lys	Leu
		515					520					525			
Met	Arg	Asn	Glu	Leu	Arg	Ala	Ile	Phe	Ala	Arg	Glu	Gln	Ala	Lys	Ser
	530					535					540				
Lys	Leu														
545															

Redline

Filename : *Phrixothrix vivianii* lateral lanterns green light-eliciting luciferase cDNA and deduced primary structure.
Sequence Size : 1746
Sequence Position: -25 - 1746

Translation Position: 1 - 1635;

Genetic Code : Universal (amino-acid residues are in 3 letter code)

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      MetGluGluGluAsnIleArgHisGlyGluArgProArgAspIleValHisPro

    60        70        80        90       100       110
GGCTCGGCAGGACAACAATTATACCAATCATTGTATAAATTTGCATCTTTTCCTGAAGCA
GlySerAlaGlyGlnGlnLeuTyrGlnSerLeuTyrLysPheAlaSerPheProGluAla

   120       130       140       150       160       170
ATAATCGATGCTCATACAAATGAAGTAATATCATATGCTCAAATATTTGAAACCAGCTGC
IleIleAspAlaHisThrAsnGluValIleSerTyrAlaGlnIlePheGluThrSerCys

   180       190       200       210       220       230
CGCTTAGCTGTTAGTATAGAACAATATGGCTTGAATGAAAACAATGTTGTGGGTGTATGC
ArgLeuAlaValSerIleGluGlnTyrGlyLeuAsnGluAsnAsnValValGlyValCys

   240       250       260       270       280       290
AGTGAAAACAATATAAACTTTTTTAATCCTGTCCTTGCTGCTTTATACTTAGGAATACCA
SerGluAsnAsnIleAsnPhePheAsnProValLeuAlaAlaLeuTyrLeuGlyIlePro

   300       310     - 320       330       340       350
GTAGCAACATCAAATGATATGTACACAGATGGAGAGTTAACTGGTCATTTGAATATATCA
ValAlaThrSerAsnAspMetTyrThrAspGlyGluLeuThrGlyHisLeuAsnIleSer

   360       370       380       390       400       410
AAACCAACTATCATGTTTAGTTCAAAGAAAGCACTCCCGCTTATTCTGAGAGTACAGCAA
LysProThrIleMetPheSerSerLysLysAlaLeuProLeuIleLeuArgValGlnGln

   420       430       440       450       460       470
AATCTAAGTTTCATTAAAAAAGTCGTAGTTATCGATAGCATGTACGACATTAATGGCGTT
AsnLeuSerPheIleLysLysValValValIleAspSerMetTyrAspIleAsnGlyVal

   480       490       500       510       520       530
GAATGCGTATCTACCTTTGTTGCACGTTATACTGACCACACCTTTGATCCATTGTCATTT
GluCysValSerThrPheValAlaArgTyrThrAspHisThrPheAspProLeuSerPhe

   540       550       560       570       580       590
ACACCAAAAGATTTTGATCCCCTTGAAAAAATCGCATTAATTATGTCATCATCTGGAACA
ThrProLysAspPheAspProLeuGluLysIleAlaLeuIleMetSerSerSerGlyThr
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FIG. 1A

600 610 620 630 640 650
ACTGGATTGCCTAAGGGTGTAGTACTGAGCCATAGAAGTCTAACTATAAGATTCGTTCAT
ThrGlyLeuProLysGlyValValLeuSerHisArgSerLeuThrIleArgPheValHis

660 670 680 690 700 710
AGCAGGGATCCCATTTATGGCACTCGTACGGTTCCACAAACATCAATTCTTTCCTTAGTA
SerArgAspProIleTyrGlyThrArgThrValProGlnThrSerIleLeuSerLeuVal

720 730 740 750 760 770
CCGTTCCATCATGCCTTTGGAATGTTTACTACATTATCTTACTTTGTAGTAGGACTTAAG
ProPheHisHisAlaPheGlyMetPheThrThrLeuSerTyrPheValValGlyLeuLys

780 790 800 810 820 830
GTTGTAATGTTGAAGAAATTTGAGGGCGCACTTTTCTTAAAAACCATACAGAATTACAAA
ValValMetLeuLysLysPheGluGlyAlaLeuPheLeuLysThrIleGlnAsnTyrLys

840 850 860 870 880 890
ATCCCCACTATTGTAGTGGCCCCTCCAGTTATGGTGTTTTTGGCTAAAAGCCCATTAGTC
IleProThrIleValValAlaProProValMetValPheLeuAlaLysSerProLeuVal

900 910 920 930 940 950
GATCAATACGATTTATCGAGCTTAACGGAAGTTGCTACTGGAGGAGCTCCTTTAGGAAAA
AspGlnTyrAspLeuSerSerLeuThrGluValAlaThrGlyGlyAlaProLeuGlyLys

960 970 980 990 1000 1010
GATGTCGCAGAAGCAGTAGCAAAGAGGTTGAAATTACCTGGAATCATACAAGGATATGGA
AspValAlaGluAlaValAlaLysArgLeuLysLeuProGlyIleIleGlnGlyTyrGly

Insert A

1020 1030 1040 1050 1060 1070
TTAACTGAAACTTGCTGCGCTGTAATGATTACCCCTCATAATGCTGTGAAAACAGGTTCA
LeuThrGluThrCysCysAlaValMetIleThrProHisAsnAlaValLysThrGlySer

1080 1090 1100 1110 1120 1130
ACTGGAAGACCCTTGCCATACATTAAAGCTAAAGTTTTAGATAACGCTACTGGAAGGCG
ThrGlyArgProLeuProTyrIleLysAlaLysValLeuAspAsnAlaThrGlyLysAla

1140 1150 1160 1170 1180 1190
CTAGGACCAGGAGAAAGAGGCGAAATATGCTTTCAAAGTGAAATGATTATGAAAGGATAT
LeuGlyProGlyGluArgGlyGluIleCysPheGlnSerGluMetIleMetLysGlyTyr

1200 1210 1220 1230 1240 1250
TACAACAATCCGGAAGCAACTATTGATACTATTGACAAAGATGGTTGGCTTCATTCTGGA
TyrAsnAsnProGluAlaThrIleAspThrIleAspLysAspGlyTrpLeuHisSerGly

1260 1270 1280 1290 1300 1310
GATATTGGATATTACGACGAAGATGGAAATTTCTTTATAGTTGATCGATTGAAAGAACTT
AspIleGlyTyrTyrAspGluAspGlyAsnPhePheIleValAspArgLeuLysGluLeu

1320 1330 1340 1350 1360 1370
ATTAAATACAAGGGATATCAGGTTGCGCCTGCTGAACTGGAAAATCTGCTTTTACAACAT
IleLysTyrLysGlyTyrGlnValAlaProAlaGluLeuGluAsnLeuLeuLeuGlnHis

1380 1390 1400 1410 1420 1430
CCAAGTATTGCTGATGCGGGTGTTACTGGAGTTCCGGACGAATTTGGTGGACAATTACCT
ProSerIleAlaAspAlaGlyValThrGlyValProAspGluPheGlyGlyGlnLeuPro

FIG. 1B

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  1440      1450      1460      1470      1480      1490
GCTGCTTGTGTTGTGTTAGAATCTGGCAAGACGCTGACTGAAAAGGAAGTTCAAGATTTT
AlaAlaCysValValLeuGluSerGlyLysThrLeuThrGluLysGluValGlnAspPhe

  1500      1510      1520      1530      1540      1550
ATTGCAGCACAAGTCACTCCAACAAAGCATCTTCGAGGCGGTGTCGTATTTGTAGACAGT
IleAlaAlaGlnValThrProThrLysHisLeuArgGlyGlyValValPheValAspSer

  1560      1570      1580      1590      1600      1610
ATTCCGAAAGGCCCTACTGGAAAACTCATCAGAAAGGAGCTCCGAGAAATATTTGCCCAG
IleProLysGlyProThrGlyLysLeuIleArgLysGluLeuArgGluIlePheAlaGln

  1620      1630      1640
CGAGCACCAAAATCAAAATTATAAGTTCAATGTATTGCTTTAGTTCTAAAATGTATATAA
ArgAlaProLysSerLysLeu***

ACAAGTTTTAGAACCTAATACATTCATTCAAATACTAAACAAAAAAAAAAAAAAAAAAA
  1740
AAAAAA
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FIG. 1C